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INITIAL RESULTS FROM THE DMS-GO INITIATIVE TO PRODUCE A NEW GLOBAL SURFACE-OCEAN DMS CLIMATOLOGY

It has been postulated that the biogenic trace gas, dimethylsulphide (DMS), may play a role in the regulation of climate. As part of the assessment of this hypothesis, it is important to quantify the global flux of DMS across the air-sea interface. A decade ago, Jamie Kettle compiled a database of available surface measurements (~15,000 data points), and used them to create global DMS concentration and flux climatologies with seasonal variability (Kettle et al. 1999). The significance of this work to the scientific community is easily demonstrated by the number of citations it has received (210 to date). However, since this landmark publication, the online database has grown substantially to ~40,000 data points, with increased spatial and temporal coverage. Working with the SOLAS Integration Project (http://www.bodc.ac.uk/solas_integration/) and COST Action 735 (http://www.cost-735.org/), DMS-GO (DiMethylSulfide concentrations and emission fluxes in the Global Ocean) is an initiative to produce new DMS climatologies from the updated database. We will present and discuss the initial results from this project, with particular emphasis on the implications of its conclusions.

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SPATIO-TEMPORAL VARIABILITY OF VIRUSES FROM PRASINOPHYTE PLANCTONIC ALGAE IN THE NORTH WEST MEDITERRANEAN SEA

Viruses are increasingly recognized to be major regulators of picophytoplanktonic populations. In the Mediterranean Sea, Mamiellales green algae are the most abundant and widespread representatives of the Prasinophyceae, especially the three genera Bathycoccus, Micromonas and Ostreococcus. We showed that Phycodnaviridae currently occurs in these algae in the Mediterranean Sea and coastal lagoons. Several methods (growth on solid medium, Fish, cytometry, phylogenetic analyses…) were used to study the diversity of viruses infecting different Ostreococcus strains in a spatio-temporal manner. Viruses were characterized and identified via the partial sequencing of the DNA polymerase gene. We isolated twenty-seven new viral strains from five different host strains. Furthermore, since 2007, time series were carried out to quantify hosts and associated viruses. We thus monitored abundance, diversity and polymorphism of algal hosts and their viruses. This study brings some insights about the evolutionary history of the picoalgal-virus system and the factors controlling these interactions.

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BACTERIAL COMMUNITIES IN MARINE BIOFILM GROWING ON ARTIFICIAL SUBSTRATA IN DEEP SEA WATERS OF THE EASTERN MEDITERRANEAN SEA

In this study terminal-restriction fragment length polymorphism (T-RFLP) fingerprinting was used to analyze the community structure of bacteria growing in biofilms attached to different types of artificial substratum deployed in the deep sea waters of the Hellenic Trench (Ionian Sea). This area is characterized by small temperature fluctuations between the deep-water layers. As a consequence, it seems relevant to examine possible variations in the community structure of bacteria with regard to depth and substratum, as other environmental factors probably determine depth zonation of bacteria. In order to test if depth and type of substratum can affect the biofilm formation and its structure in terms of bacterial communities in deep-sea biofilms, an innovative experimental device with five different types of artificial substratum (titanium, aluminum, glass, limestone and shale) were deployed for a six month period at four different depths (4500, 3500, 2500 and 1500m) at the Hellenic Trench. The analyses of 64 T-RFLP-electropherograms displayed differences among depths and thus indicate that within one deep-sea water layer the physical nature of surfaces affects the settlement of bacteria as shown in coastal areas

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MODELLING THE BIOGEOCHEMICAL CYCLES IN THE MEDITERRANEAN SEA

The Mediterranean Sea is generally regarded as the best site to understand the interactions between the climate, the biogeochemical cycles as well as the marine ecosystems (Béthoux et al., 1999), because of its short turnover time of water and zones of deep water formation. Many studies have observed physical modifications (Rother and al., 1998) as well as biological ones (Marty and Chiavérini, 2002) which could be partially explained by climatic changes (Béthoux et al., 2001). It appears hence necessary to evaluate the impact of climate anomalies on biogeochemical fluxes in the Mediterranean Sea. To this end, I am adapting the biogeochemical model of the global ocean (LOCH) developed by Mouchet et François (1996) and coupling it to the GHER 3D circulation model of the Mediterranean Sea (Beckers et al., 2002). The biogeochemical module contains 9 states variables (2 groups of phytoplankton, silicate, biogenic silica, phosphorus, alkalinity, dissolved inorganic carbon, dissolved and particulate organic matter). We run the model forced with climatological forcing in order to reproduce the seasonal distribution of the biogeochemical fluxes over the whole Mediterranean Sea. The results will be presented and discussed. We also compare the distribution of pCO2 obtained with the model to in situ pCO2 data in different sampling stations of the Mediterranean Sea (e.g Dyfamed).

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ALTERATION OF OCEANIC NITRIFICATION UNDER ELEVATED CARBON DIOXIDE CONCENTRATIONS

Dissolution of anthropogenic carbon dioxide (CO_2) in the ocean reduces pH, alters carbonate chemistry, and also represents a potential resource for a broad spectrum of marine microorganisms that fix inorganic carbon. These bacteria and archaea drive global biogeochemical cycles of carbon and nitrogen, yet their responses to increased pCO_2 and reduced pH remain largely undocumented. Here we show that elevated pCO_2 may alter nitrification rates and populations of nitrifying microorganisms in the ocean. Multiple experiments were performed in the Sargasso Sea and Southern California Bight under glacial maximum (193 ppm), present day (390 ppm), and projected (750 ppm) pCO_2 concentrations, over time scales from hours to days, and at depths of 45-240 m. In the majority of experiments, populations of ammonia-oxidizing archaea and bacteria decreased by 40-80% under elevated pCO_2, and this reduction became more pronounced with exposure over time. Nitrification rates were measured with isotopically-labeled nitrogen and also showed significant responses to changes in pCO_2. These findings suggest that projected increases in pCO_2 and subsequent decreases in pH may affect microbial community structure and biogeochemistry in the sea.

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EFFECTS OF NITROGEN SOURCE AND THE LIGHT:DARK CYCLE ON GROWTH AND GENE EXPRESSION ASSOCIATED WITH THE UREA CYCLE IN THALASSIOSIRA PSEUDONANA

Whole genome sequence analysis indicates that diatoms possess a complete urea cycle. The specific function of the urea cycle in diatoms is unknown, but it has been hypothesized to connect several vital cellular pathways to one another including carbon fixation, energy storage and photorespiration. The planktonic diatom Thalassiosira pseudonana was grown in steady state on three nitrogen sources (urea, nitrate, ammonium) under a light:dark cycle. Growth rates and variable fluorescence were monitored, and differential gene expression of three key genes (CPSIII, URE, CK) associated with N-metabolism and the urea cycle was measured using quantitative PCR. Cells grew at similar rates on ammonium and nitrate; however, growth on urea was significantly elevated. Our gene expression results indicate that the first gene in the urea cycle pathway (CPSIII) is up regulated during the dark cycle relative to the light cycle. Additionally, the expression data for each gene varied based on N source. These results help clarify the function of the urea cycle in T. pseudonana, and they suggest a connection between the urea cycle and metabolic processes that occur in the dark.

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STREAM DRYING IN THE IBERIAN PENINSULA AND CONSEQUENCES FOR FISH ASSEMBLAGES

Excessive freshwater abstraction impairs the capacity of streams to support native biota. We investigated the flow regime and related variables in six river basins of the Iberian Peninsula and show that they have been strongly altered, with negative trends for flow and aquifer levels during the 20th century. We observed lower flows and higher frequency of stream-drying than those predicted by the official hydrological model used in this region. We also observed dry conditions for some streams predicted by the model to be permanently flowing. Meanwhile, there has been no decrease in precipitation. We investigated the fish assemblage of a stream in one of these river basins (Tordera) for six years and show that sites more affected by water abstraction display significant differences in four fish metrics (catch per unit effort, number of benthic species, number of intolerant species and proportional abundance of intolerant individuals). We discuss the utility of these metrics in assessing impacts of water abstraction and point out the